FIG. 1

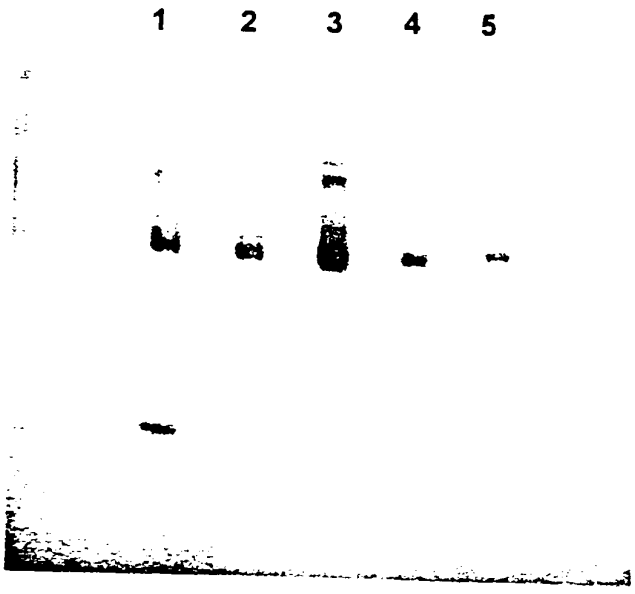


FIG. 2

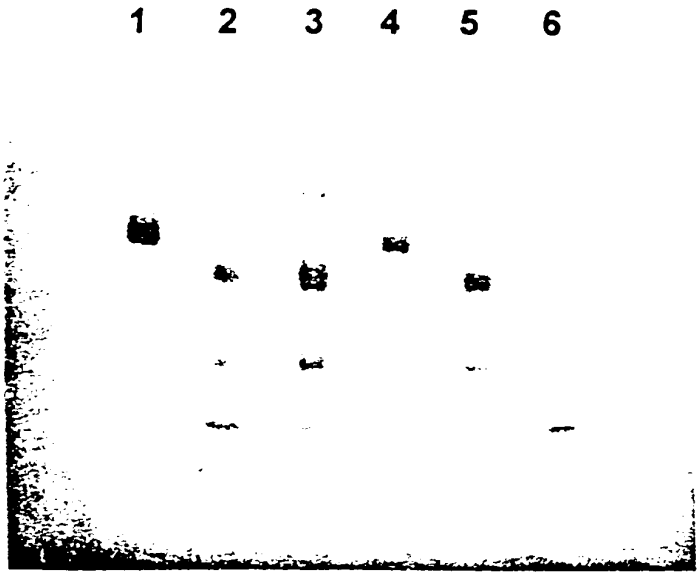


FIG. 3

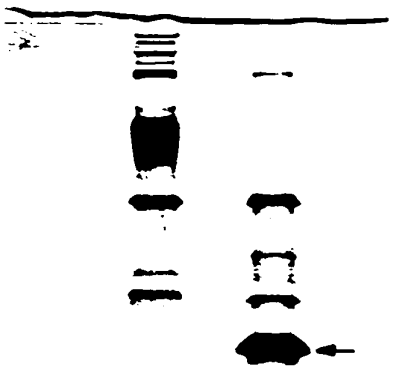


FIG. 4

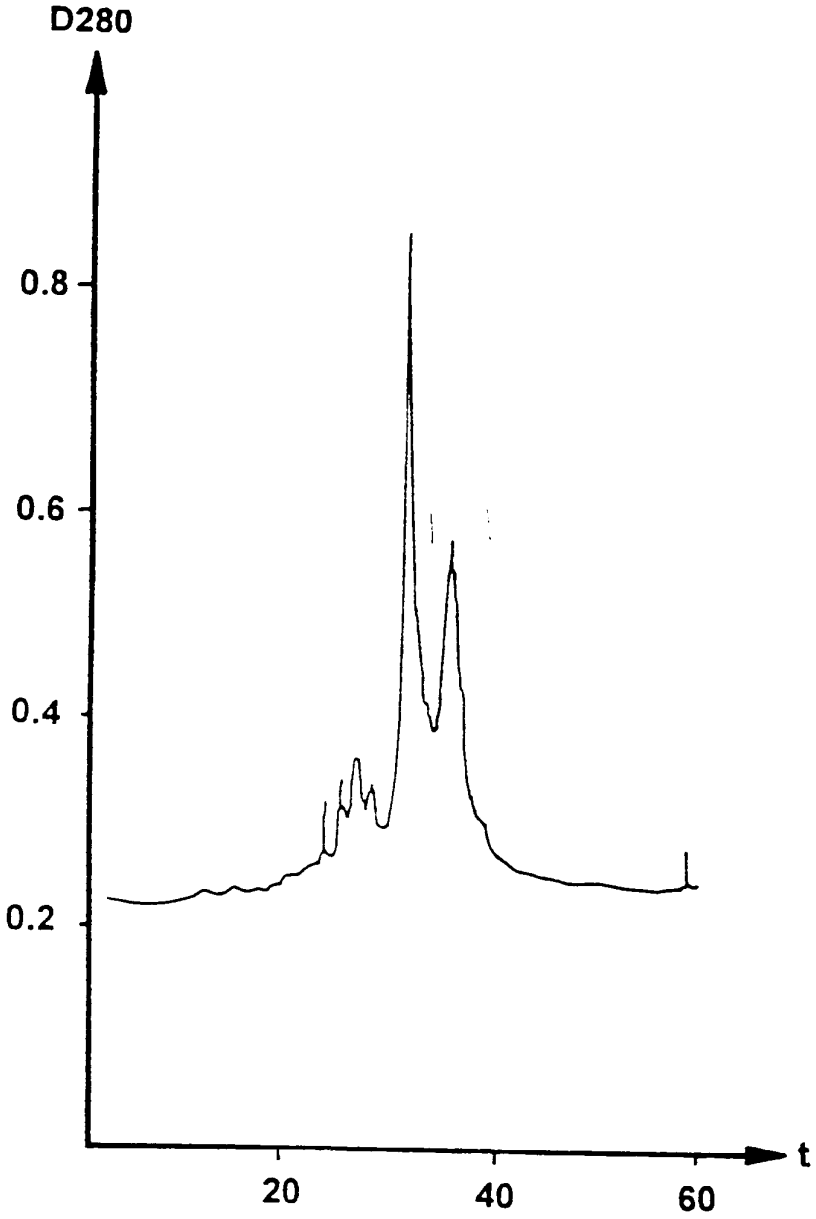


FIG. 5

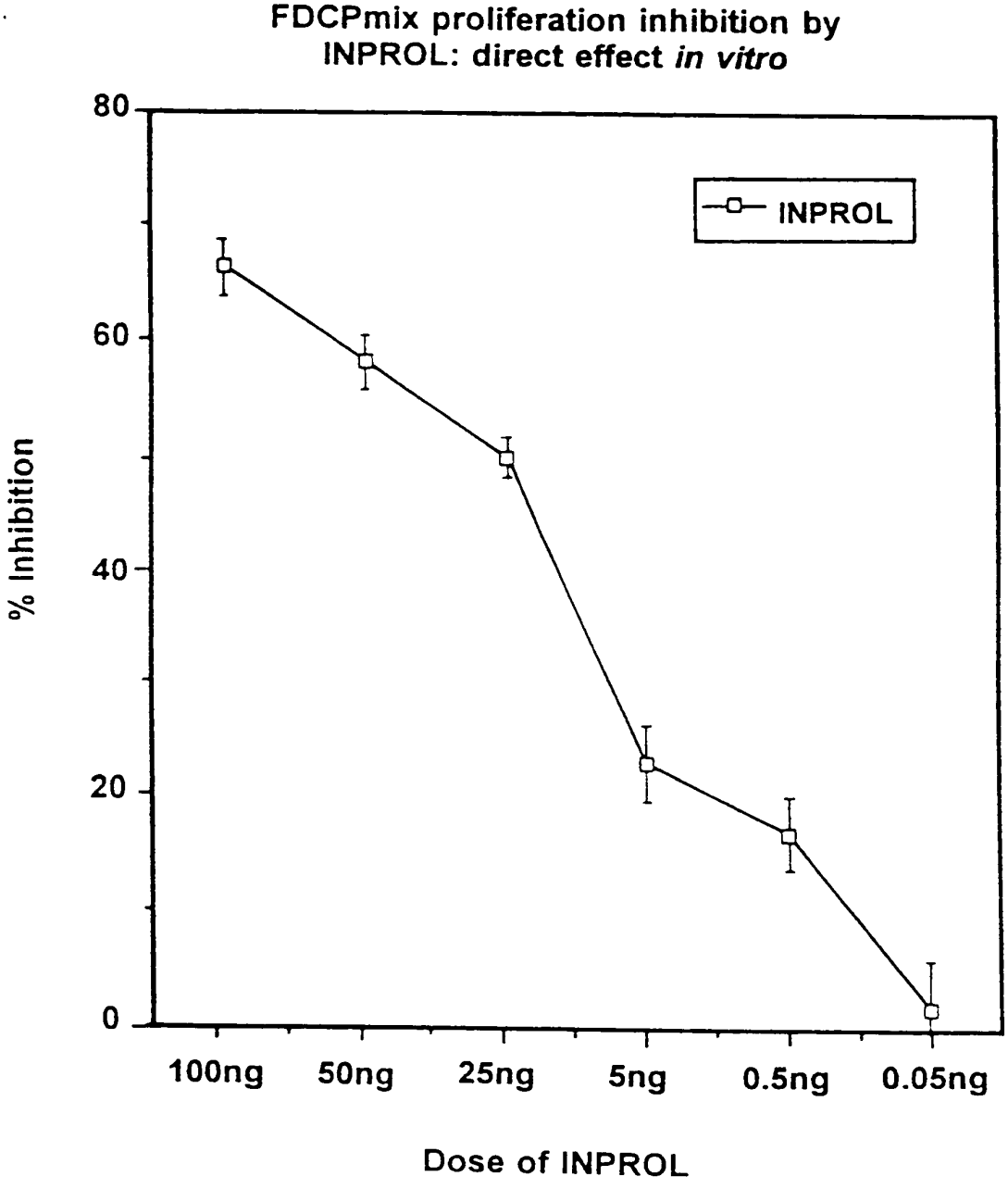

FDCPmix proliferation inhibition by INPROL: direct effect *in vitro*
INPROL
% Inhibition
80
60
40
20
0
100ng
50ng
25ng
5ng
0.5ng
0.05ng
Dose of INPROL

FIG. 6

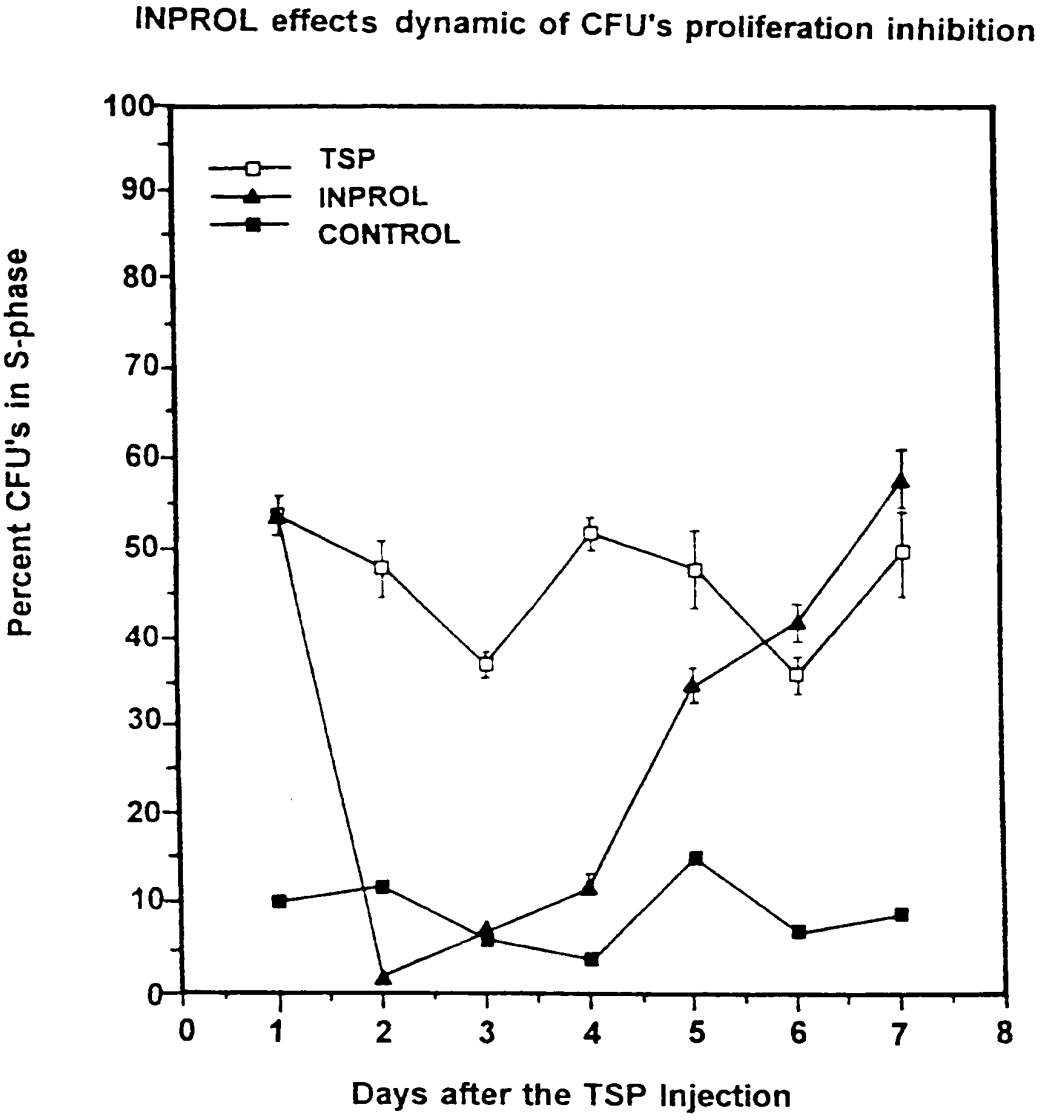
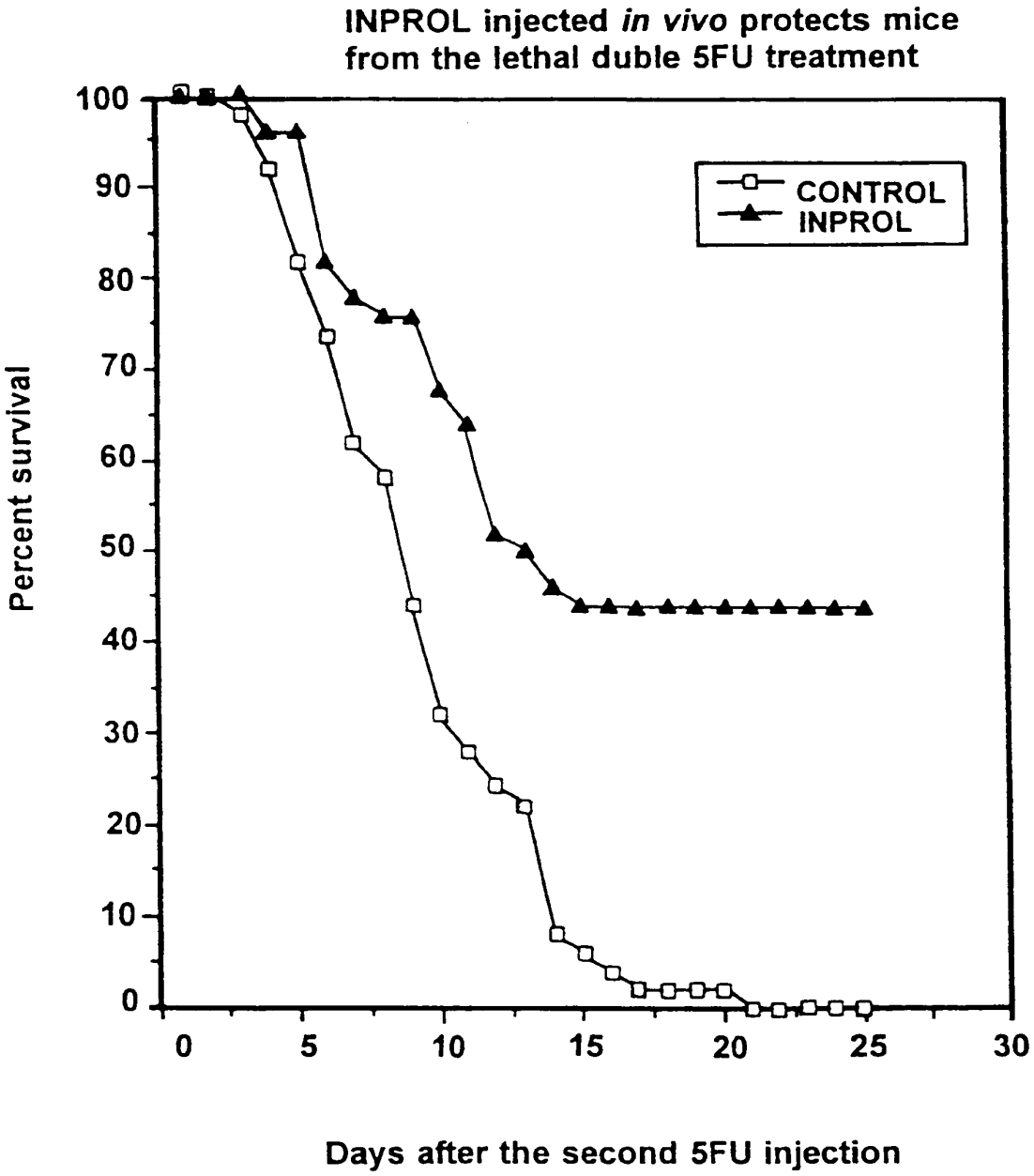

INPROL effects dynamic of CFU's proliferation inhibition
TSP
INPROL
CONTROL
Percent CFU's in S-phase
Days after the TSP Injection
0
10
20
30
40
50
60
70
80
90
100
0
1
2
3
4
5
6
7
8

FIG. 7

FIG. 8


INPROL injected *in vivo* protects mice from the lethal duble 5FU treatment
Percent survival
100
90
80
70
60
50
40
30
20
10
0
0
5
10
15
20
25
30
CONTROL
INPROL
Days after the second 5FU injection

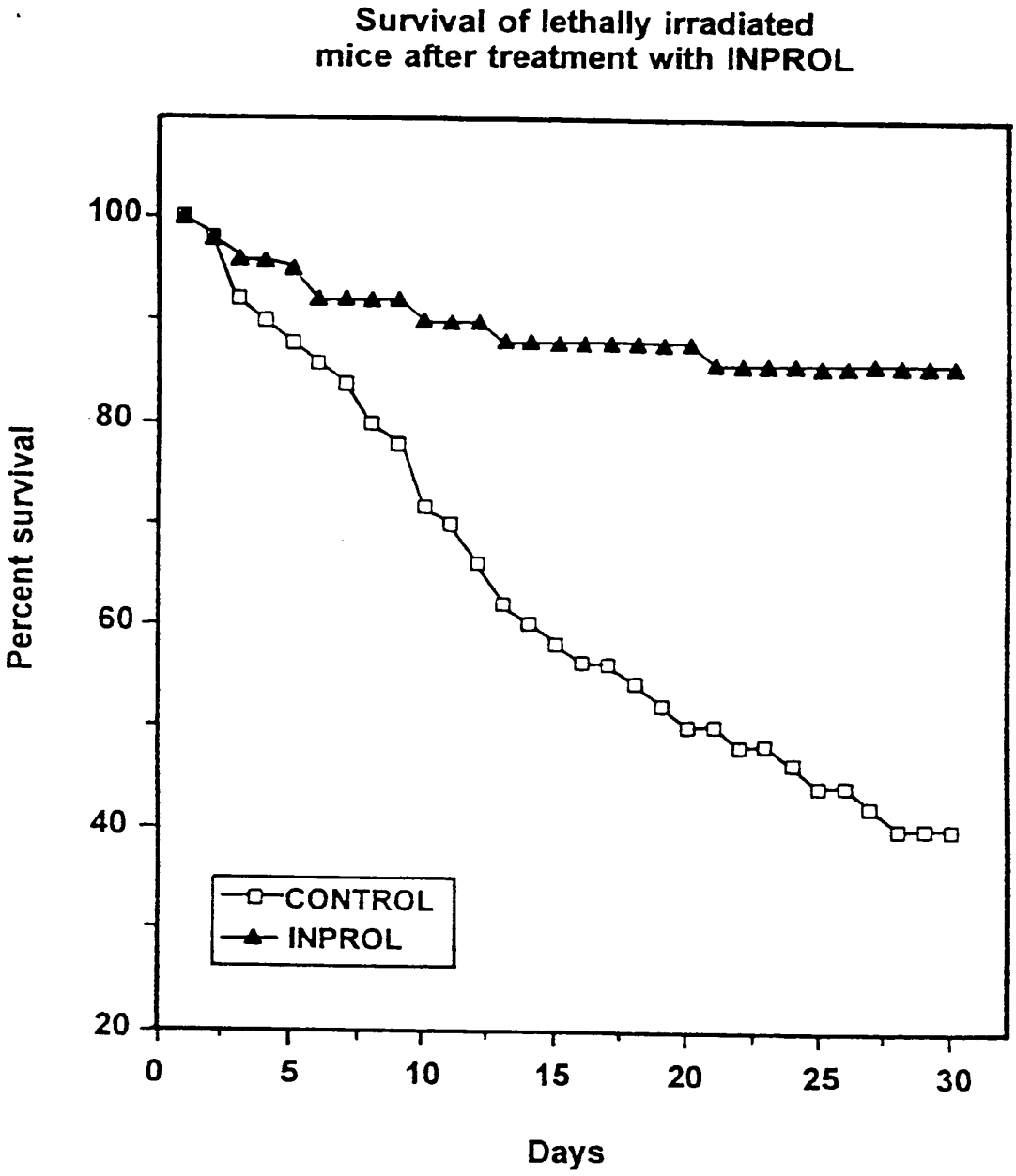

Survival of lethally irradiated
mice after treatment with INPROL
Percent survival
100
80
60
40
20
0
5
10
15
20
25
30
Days
CONTROL
INPROL

FIG. 9

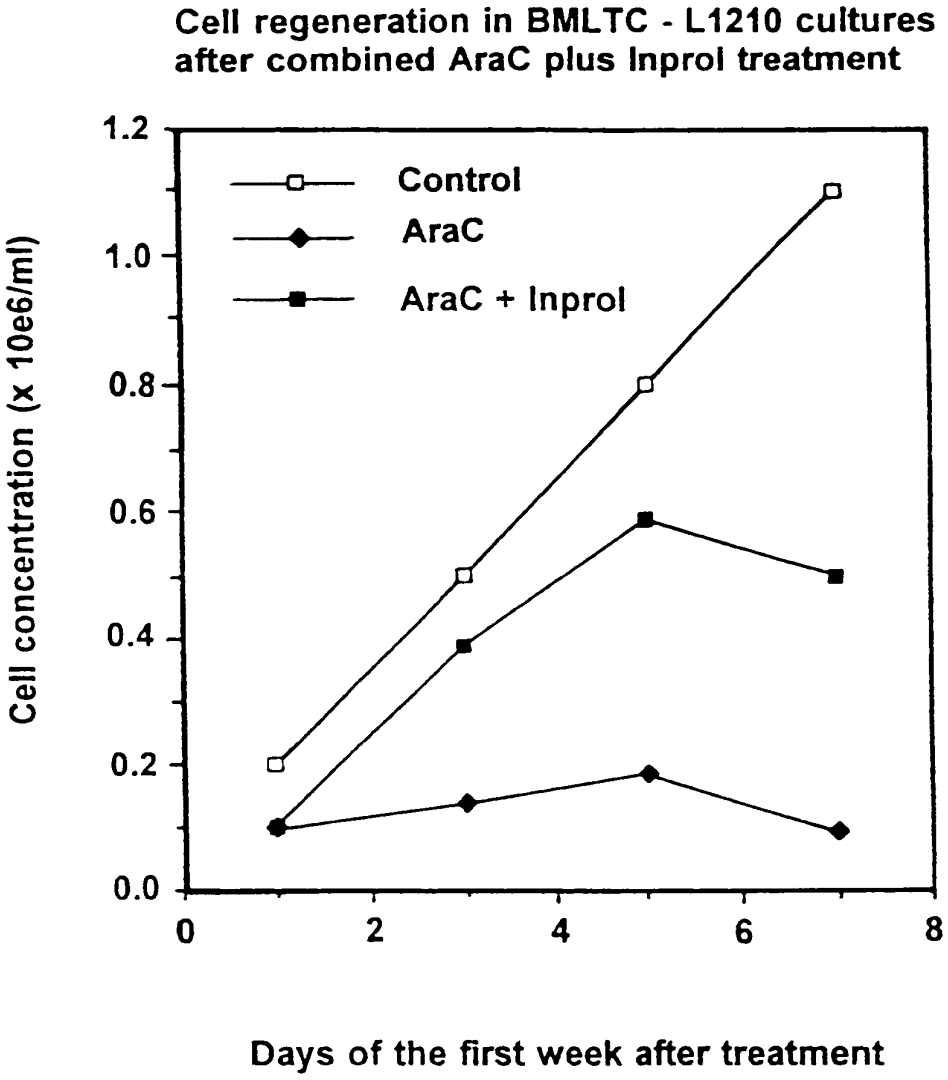

Cell regeneration in BMLTC - L1210 cultures after combined AraC plus Inprol treatment
Control
AraC
AraC + Inprol
Cell concentration (x 10e6/ml)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
2
4
6
8
Days of the first week after treatment

FIG. 10A

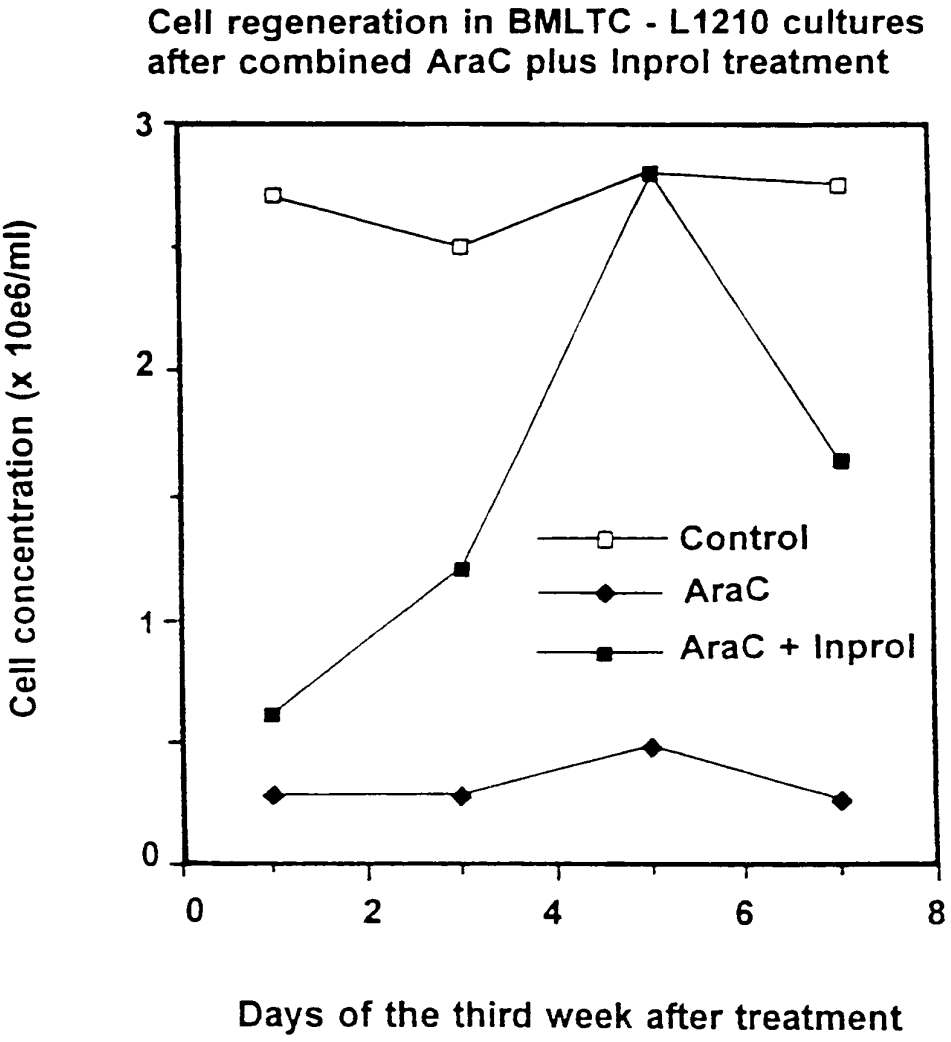

Cell regeneration in BMLTC - L1210 cultures after combined AraC plus Inprol treatment
Cell concentration (x 10e6/ml)
3
2
1
0
0
2
4
6
8
Control
AraC
AraC + Inprol
Days of the third week after treatment

FIG. 10B

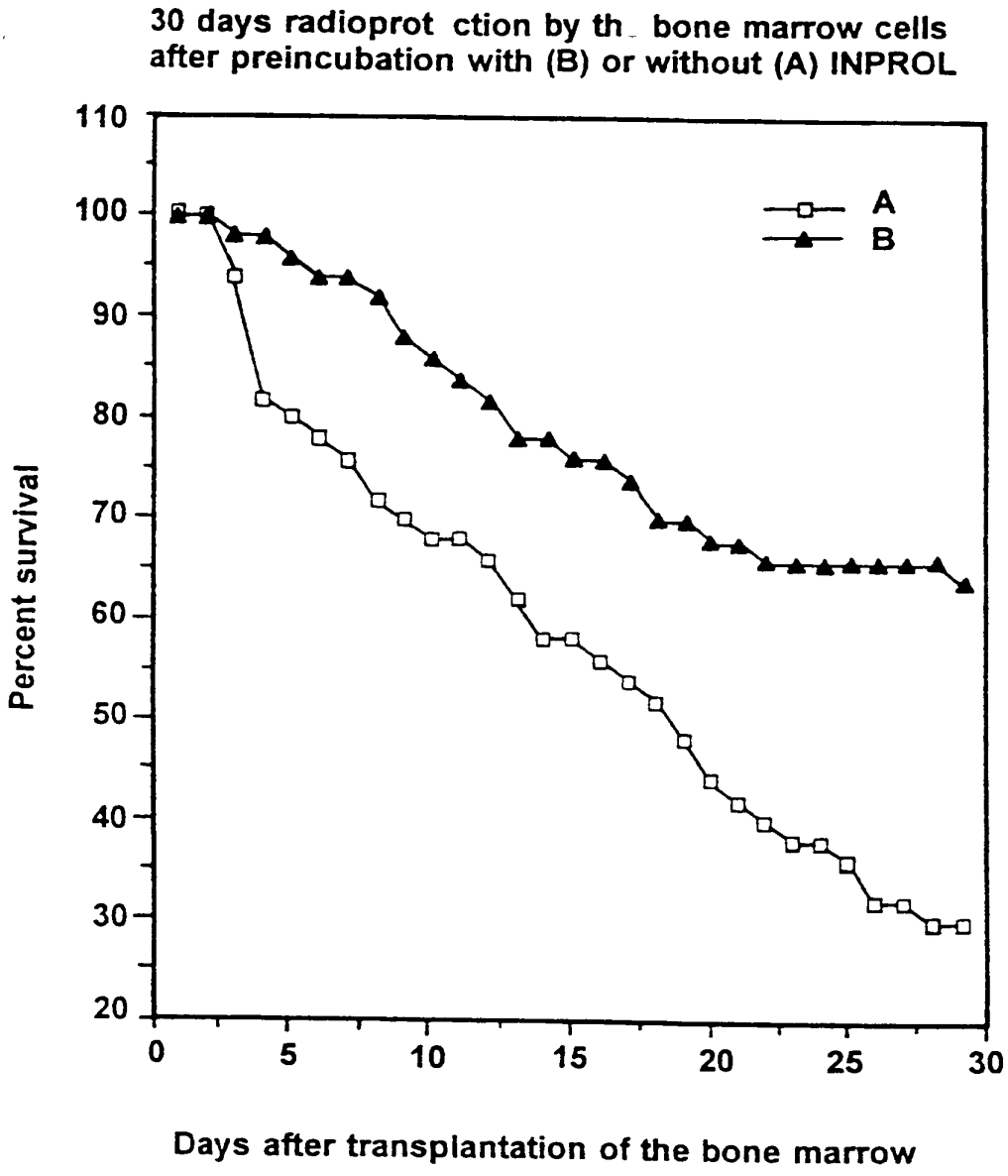

30 days radioprot ction by th bone marrow cells
after preincubation with (B) or without (A) INPROL
Percent survival
110
100
90
80
70
60
50
40
30
20
0
5
10
15
20
25
30
A
B
Days after transplantation of the bone marrow

FIG. 11

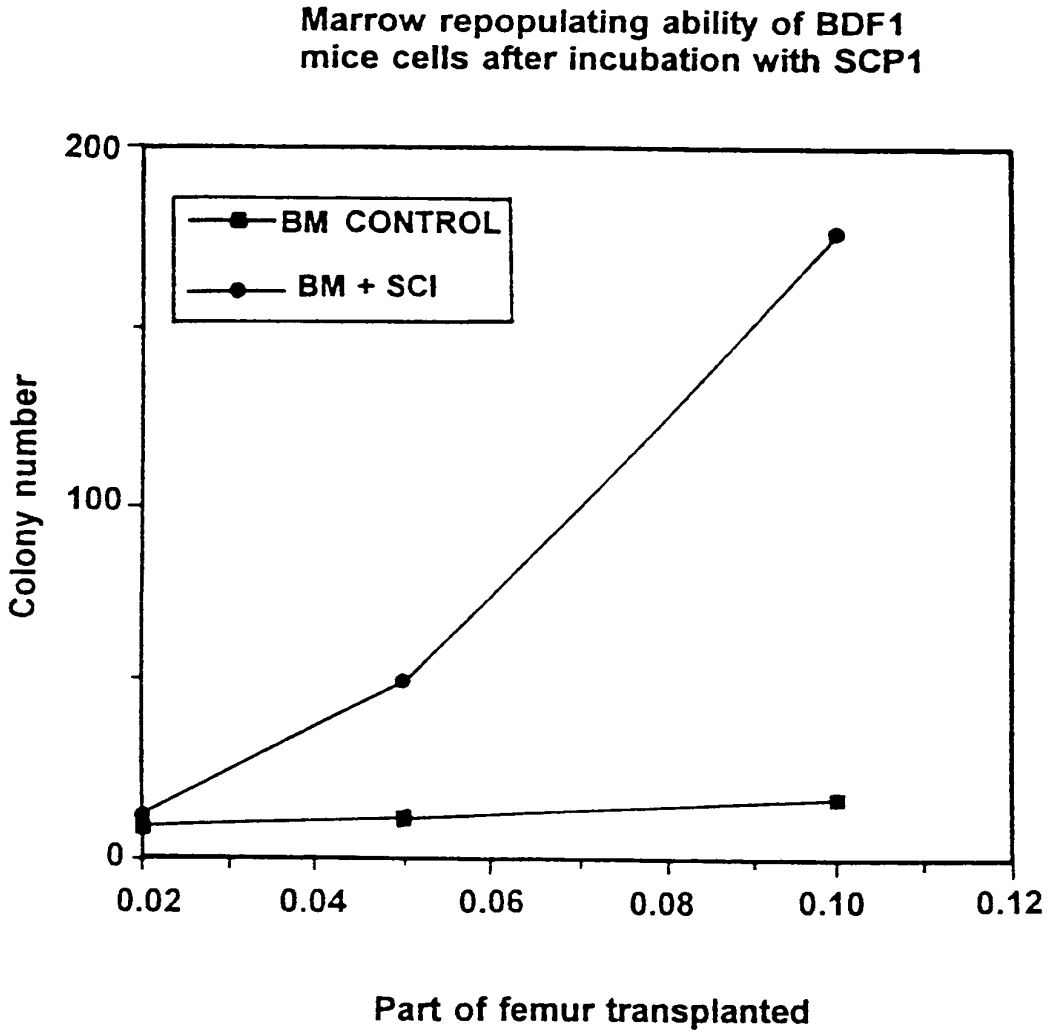

Marrow repopulating ability of BDF1 mice cells after incubation with SCP1
200
100
0
Colony number
BM CONTROL
BM + SCI
0.02
0.04
0.06
0.08
0.10
0.12
Part of femur transplanted

FIG. 12

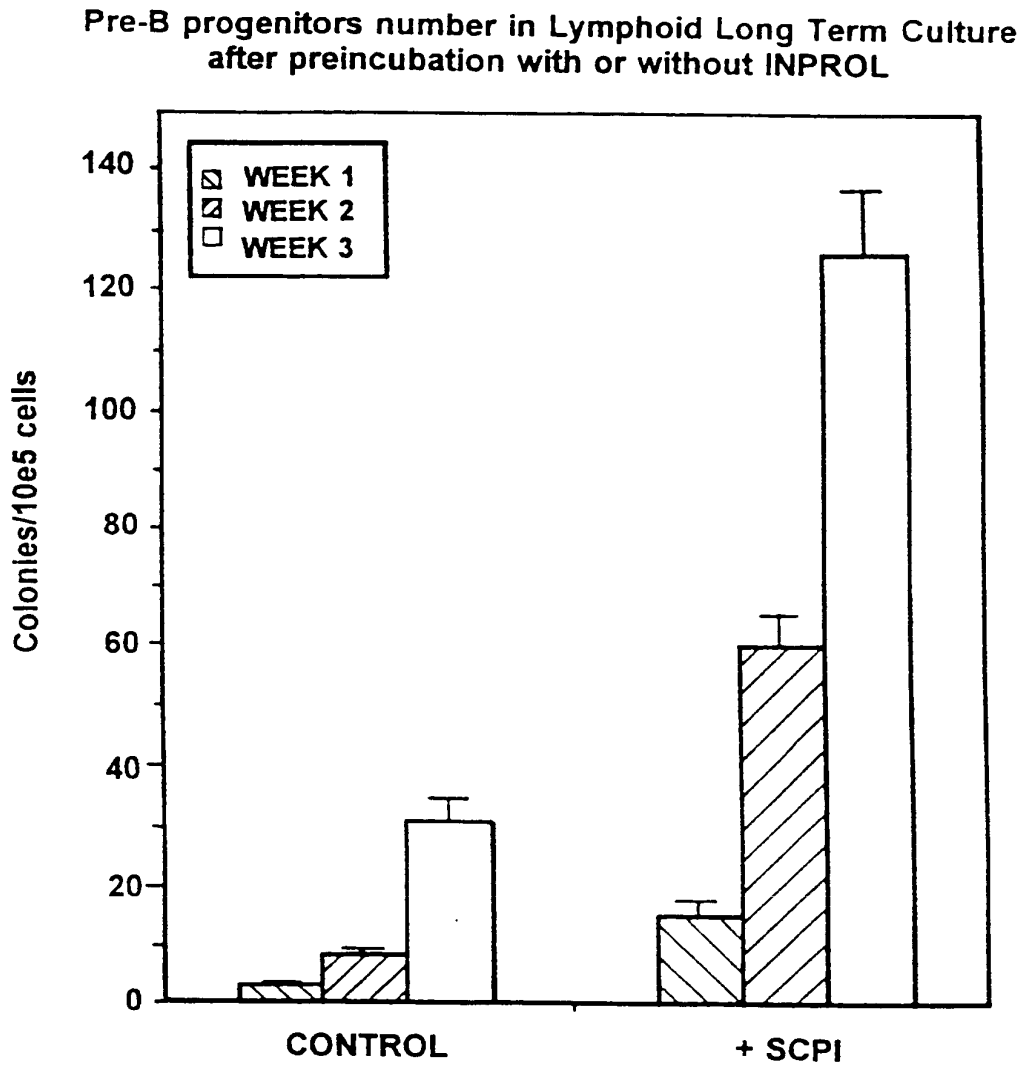
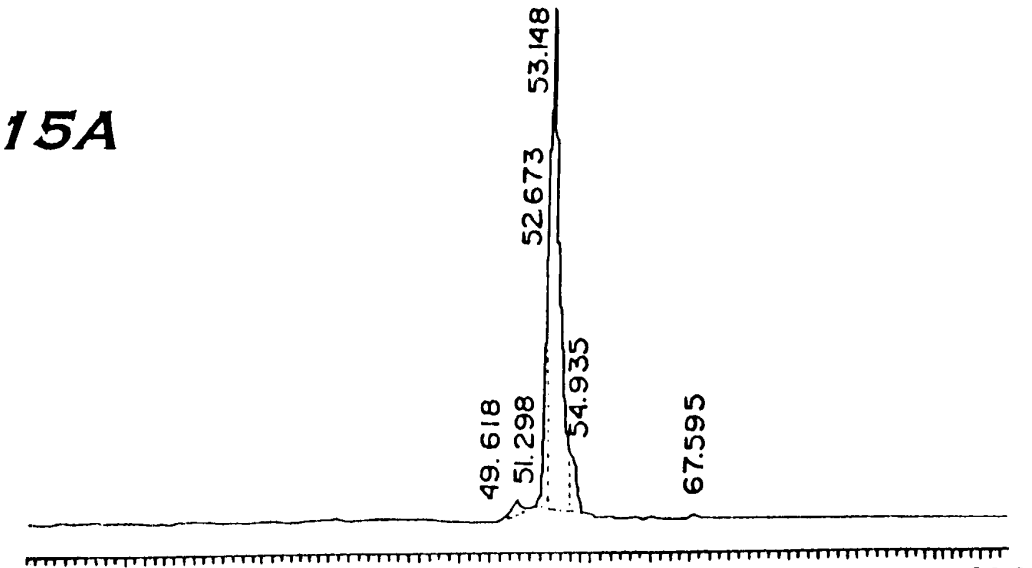

Pre-B progenitors number in Lymphoid Long Term Culture
after preincubation with or without INPROL
WEEK 1
WEEK 2
WEEK 3
Colonies/10e5 cells
140
120
100
80
60
40
20
0
CONTROL
+ SCPI

FIG. 13

FIG. 15A



Analysis: Channel A

Peak No.	Time	Type	Height(μY)	Area(μY-sec)	Area%
	3.126	N1	691	7578	0.041
	3.315	N2	1011	5150	0.027
1	49.618	N	8584	349227	1.893
2	51.298	N	1456	20274	0.109
3	52.673	N1	138069	2633395	14.278
4	53.148	N2	271587	14050458	76.181
5	54.935	N3	33016	1332820	7.226
6	67.595	N	3270	44507	0.241
TOTAL AREA				18443409	99.996

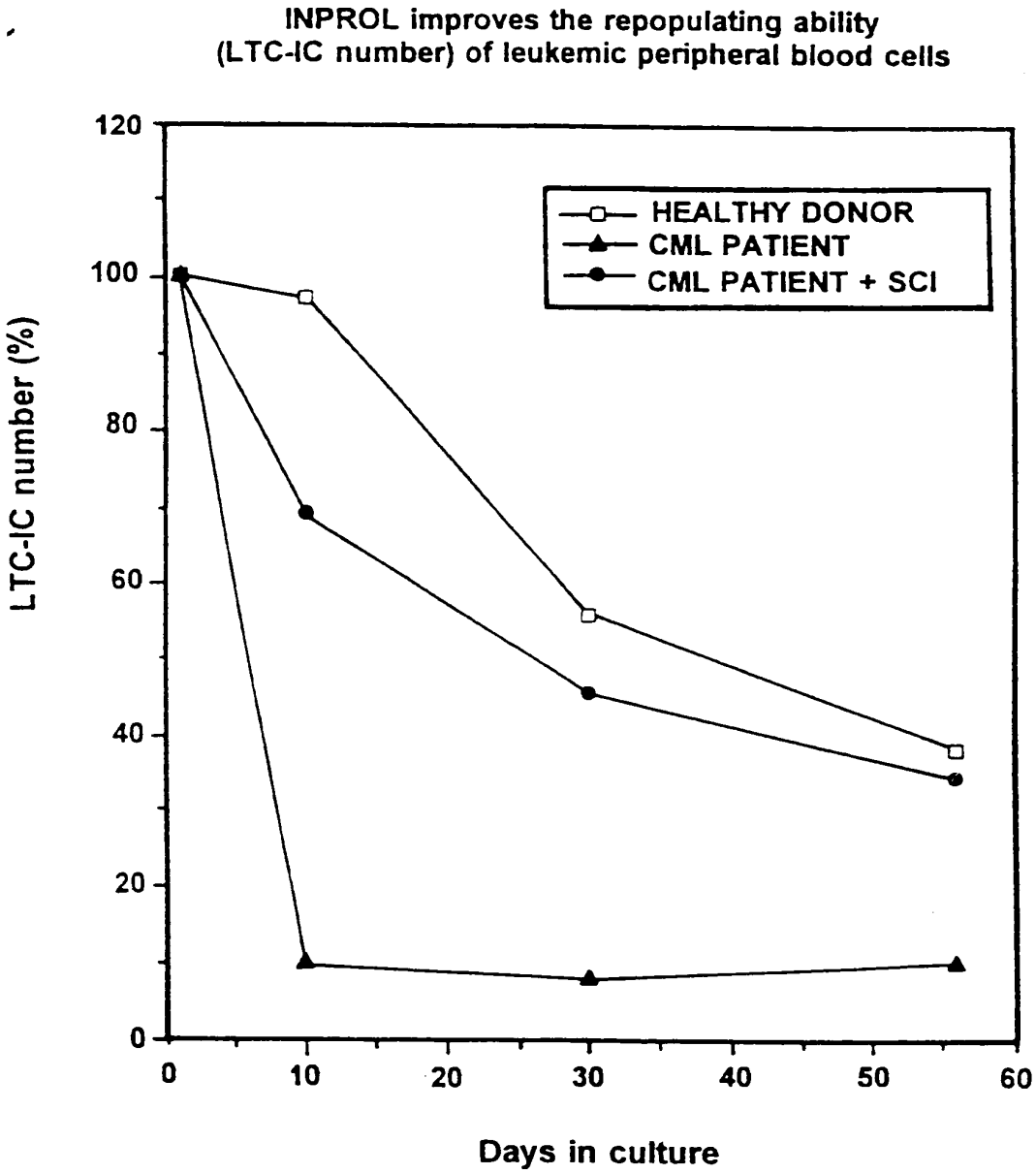
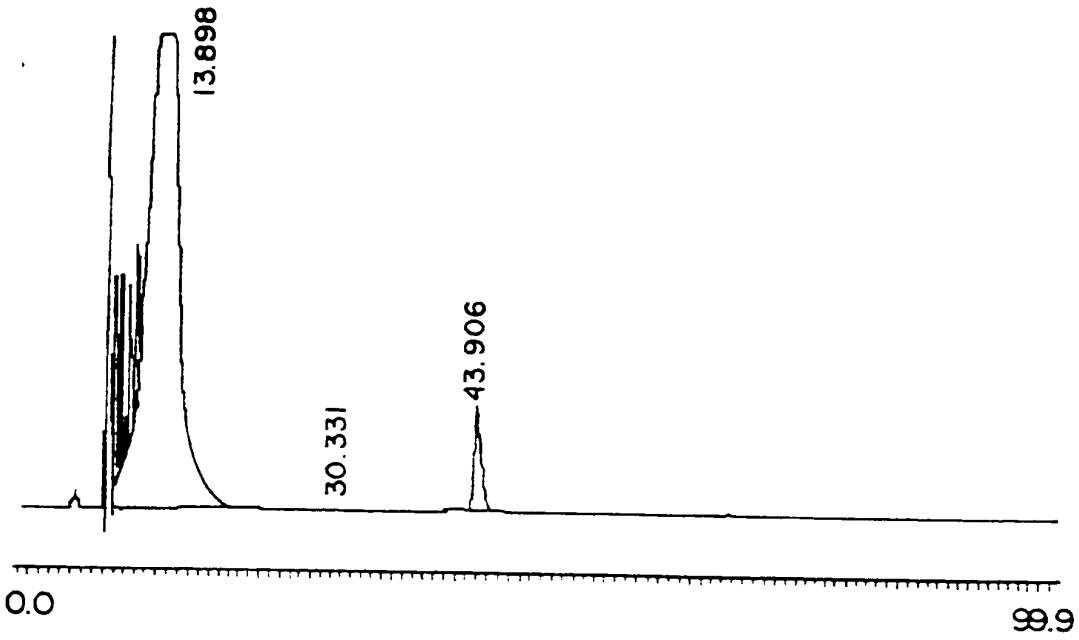

INPROL improves the repopulating ability
(LTC-IC number) of leukemic peripheral blood cells
HEALTHY DONOR
CML PATIENT
CML PATIENT + SCI
LTC-IC number (%)
120
100
80
60
40
20
0
0
10
20
30
40
50
60
Days in culture

FIG. 14



Analysis: Channel A

Peak No.	Time	Type	Height(μY)	Area(μY-sec)	Area%
1	4.383	N1	3945	95125	0.119
2	5.080	N2	28639	330889	0.413
3	5.216	N3	49084	531867	0.665
4	7.980	N1	399424	1110511	1.389
5	8.100	Err	1203320	2882013	3.605
6	8.241	N3	443249	1506159	1.884
7	8.386	N4	481563	2185702	2.734
8	8.533	N5	412886	1826165	2.284
9	8.701	N6	321500	842122	1.053
10	8.745	N7	404661	1610380	2.014
11	8.995	N8	435765	2489721	3.114
12	9.316	N9	517790	4801831	6.007

FIG. 15B

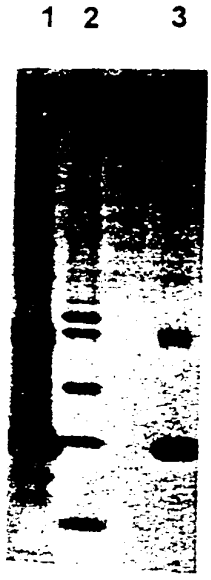


FIG. 15C

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Val	Leu	Ser	Pro	Ala	Asp	Lys	Thr	Asn	Val	Lys	Ala	Ala	Trp	Gly	Lys	Val	Gly	Ala	His
GTG	CTG	TCT	CCT	GCC	GAC	AAG	ACC	AAC	GTC	AAG	GCC	GCC	TGG	GGT	AAG	GTC	GGC	GCG	CAC

21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
Ala	Gly	Glu	Tyr	Gly	Ala	Glu	Ala	Leu	Glu	Arg	Met	Phe	Leu	Ser	Phe	Pro	Thr	Thr	Lys
GCT	GGC	GAG	TAT	GGT	GCG	GAG	GCC	CTG	GAG	AGg	ATG	TTC	CTG	TCC	TTC	CCC	ACC	ACC	AAG

41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Thr	Tyr	Phe	Pro	His	Phe	Asp	Leu	Ser	His	Gly	Ser	Ala	Gln	Val	Lys	Gly	His	Gly	Lys
ACC	TAC	TTC	CCG	CAC	TTC	GAC	CTG	AGC	CAC	GGC	TCT	GCC	CAG	GTT	AAG	GGC	CAC	GGC	AAG

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
Lys	Val	Ala	Asp	Ala	Leu	Thr	Asn	Ala	Val	Ala	His	Val	Asp	Asp	Met	Pro	Asn	Ala	Leu
AAG	GTG	GCC	GAC	GCG	CTG	ACC	AAC	GCC	GTG	GCG	CAC	GTG	GAC	GAC	ATG	CCC	AAC	GCG	CTG

81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Ser	Ala	Leu	Ser	Asp	Leu	His	Ala	His	Lys	Leu	Arg	Val	Asp	Pro	Val	Asn	Phe	Lys	Leu
TCC	GCC	CTG	AGC	GAC	CTG	CAC	GCG	CAC	AAG	CTT	CGG	GTG	GAC	CCG	GTC	AAC	TTC	AAG	CTC

101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Leu	Ser	His	Cys	Leu	Leu	Val	Thr	Leu	Ala	Ala	His	Leu	Pro	Ala	Glu	Phe	Thr	Pro	Ala
CTA	AGC	CAC	TGC	CTG	CTG	GTG	ACC	CTG	GCC	GCE	CAC	CTC	CCC	GCC	GAG	TTC	ACC	CCT	GCG

121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141
Val	His	Ala	Ser	Leu	Asp	Lys	Phe	Leu	Ala	Ser	Val	Ser	Thr	Val	Leu	Thr	Ser	Lys	Tyr	Arg
GTG	CAC	GCC	TCC	CTG	GAC	AAG	TTC	CTG	GCT	TCT	GTG	AGC	ACC	GTG	CTG	ACC	TCC	AAA	TAC	CGT

Fig. 16A

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Val	His	Leu	Thr	Pro	Glu	Glu	Lys	Ser	Ala	Val	Thr	Ala	Leu	Trp	Gly	Lys	Val	Asn	Val
GTG	CAC	CTG	ACT	CCT	GAG	GAG	AAG	TCT	GCC	GTT	ACT	GCC	CTG	TGG	GGC	AAG	GTG	AAC	GTG

21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
Asp	Glu	Val	Gly	Gly	Glu	Ala	Leu	Gly	Arg	Leu	Leu	Val	Val	Tyr	Pro	Trp	Thr	Gln	Arg
GAT	GAA	GTT	GGT	GGT	GAG	GCC	CTG	GGC	AGg	CTG	CTG	GTG	GTC	TAC	CTT	TGG	ACC	CAG	AGG

41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Phe	Phe	Glu	Ser	Phe	Gly	Asp	Leu	Ser	Thr	Pro	Asp	Ala	Val	Met	Gly	Asn	Pro	Lys	Val
TTC	TTT	GAG	TCC	TTT	GGG	GAT	CTG	TCC	ACT	CCT	GAT	GCT	GTg	ATG	GGC	AAC	CCT	AAG	GTG

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
Lys	Ala	His	Gly	Lys	Lys	Val	Leu	Gly	Ala	Phe	Ser	Asp	Gly	Leu	Ala	His	Leu	Asp	Asn
AAG	GCT	CAT	GGC	AAG	AAA	GTG	CTC	GGT	GCC	TTT	AGT	GAT	GGC	CTG	GCT	CAC	CTG	GAC	AAC

81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Leu	Lys	Gly	Thr	Phe	Ala	Thr	Leu	Ser	Glu	Leu	His	Cys	Asp	Lys	Leu	His	Val	Asp	Pro
CTG	AAG	GGC	ACC	TTT	GCC	ACA	CTG	AGT	GAG	CTG	CAC	TGT	GAC	AAG	CTG	CAC	GTG	GAT	CCT

101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Glu	Asn	Phe	Arg	Leu	Leu	Gly	Asn	Val	Leu	Val	Cys	Val	Leu	Ala	His	His	Phe	Gly	Lys
GAG	AAC	TTC	AGG	CTG	CTG	GGC	AAC	GTG	CTG	GTC	TGT	GTG	CTG	GCC	CAT	CAC	TTT	GGC	AAA

121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140
Glu	Phe	Thr	Pro	Pro	Val	Gln	Ala	Ala	Tyr	Gln	Lys	Val	Val	Ala	Gly	Val	Ala	Asn	Ala
GAA	TTC	ACC	CCA	CCA	GTG	CAG	GCT	GCC	TAT	CAG	AAA	GTG	GTG	GCT	GGT	GTG	GCT	AAT	GCC

141	142	143	144	145	146
Leu	Ala	His	Lys	Tyr	His
CTG	GCC	CAC	AAG	TAT	CAC

Fig. 16B

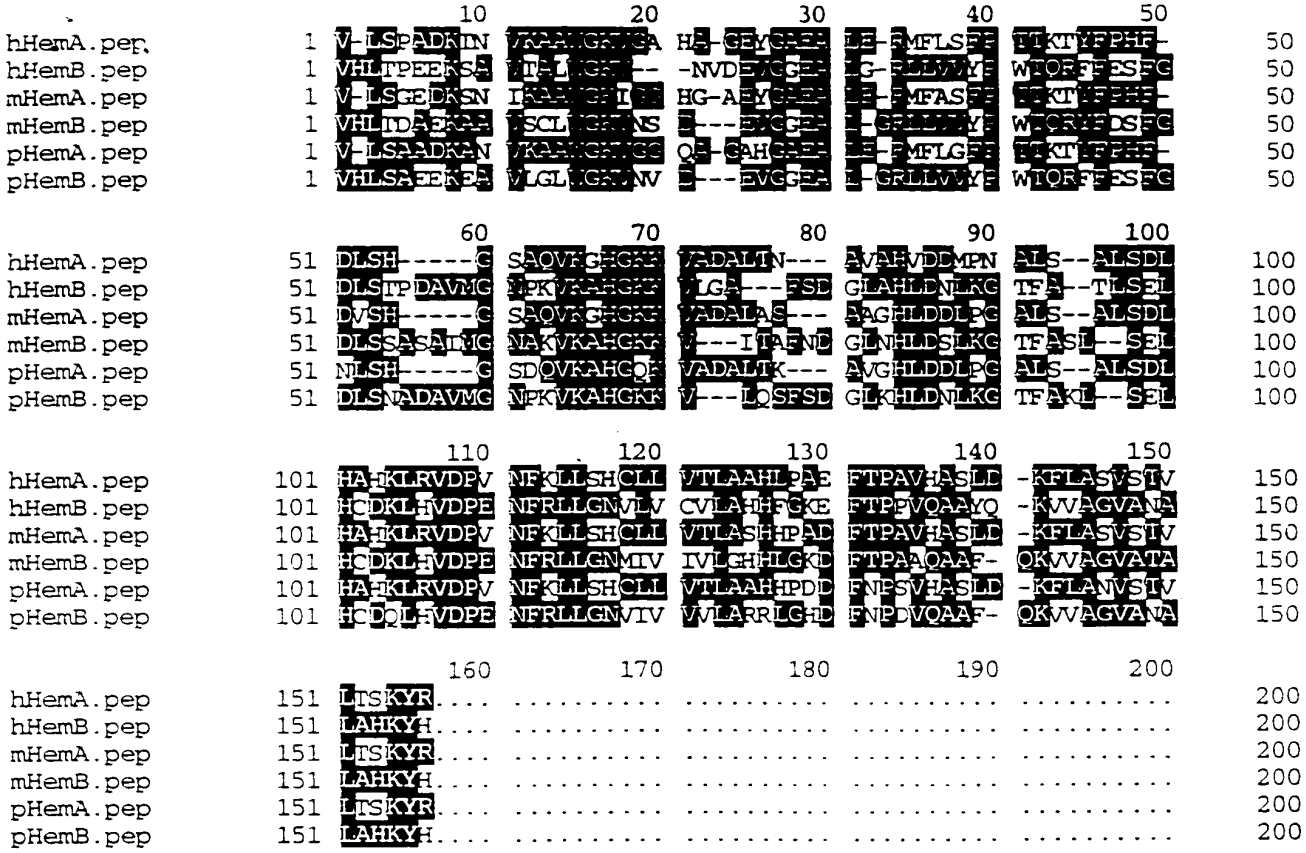
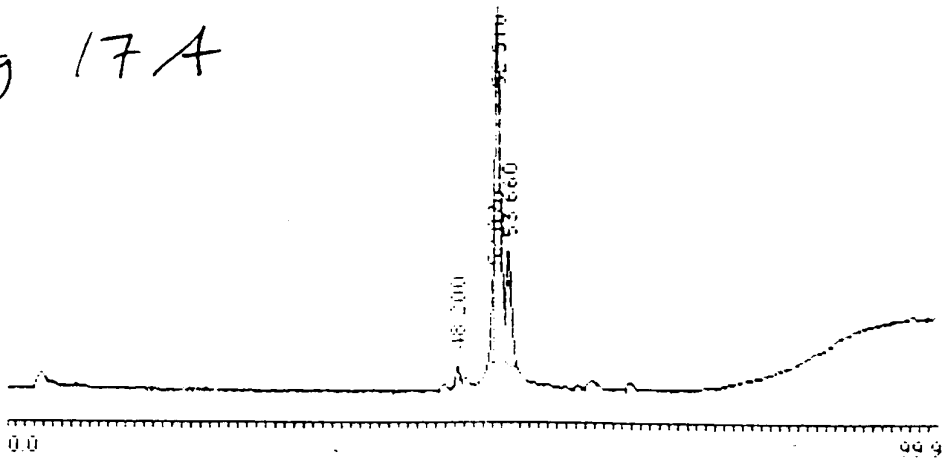

10 20 30 40 50
hHemA.pep 1 V-LSPADKTN VKAAWGKVGA HA-GEYGAEA LE-RMFLSFP TTKTYFPHF- 50
hHemB.pep 1 VHLTPEEKSA VTALWGKV-- -NVDEVGGEA LG-RLLVVYP WTQRFFESFG 50
mHemA.pep 1 V-LSGEDKSN IKAAWGKIGG HG-AEYGAEA LE-RMFASFP TTKTYFPHF- 50
mHemB.pep 1 VHLTDAEKAA VSCLWGKVNS D---EVGGEA LGRLLVVYP WTQRFFDSFG 50
pHemA.pep 1 V-LSAADKAN VKAAWGKVGG QA-GAHGAEA LE-RMFLGFP TTKTYFPHF- 50
pHemB.pep 1 VHLSAEEKEA VLGLWGKVNV D---EVGGEA LGRLLVVYP WTQRFFESFG 50
60 70 80 90 100
hHemA.pep 51 DLSH-----G SAQVKGHGKK VADALTN--- AVAHVDDMPN ALS--ALSDL 100
hHemB.pep 51 DLSTPDAVMG NPKVKAHGKK VLGA---FSD GLAHLDNLKG TFA--TLSEL 100
mHemA.pep 51 DVSH-----G SAQVKGHGKK VADALAS--- AAGHLDDLPG ALS--ALSDL 100
mHemB.pep 51 DLSSASAIMG NAKVKAHGKK V---ITAFND GLNHLDSLKG TFASL--SEL 100
pHemA.pep 51 NLSH-----G SDQVKAHGQK VADALTK--- AVGHLDDLPG ALS--ALSDL 100
pHemB.pep 51 DLSNADAVMG NPKVKAHGKK V---LQSFSD GLKHLDNLKG TFAKL--SEL 100
110 120 130 140 150
hHemA.pep 101 HAHKLRVDPV NFKLLSHCLL VTLAAHLPAE FTPAVHASLD -KFLASVSTV 150
hHemB.pep 101 HCDKLHVDPE NFRLLGNVLV CVLAHHFGKE FTPPVQAAYQ -KVVAGVANA 150
mHemA.pep 101 HAHKLRVDPV NFKLLSHCLL VTLASHHPAD FTPAVHASLD -KFLASVSTV 150
mHemB.pep 101 HCDKLHVDPE NFRLLGNMIV IVLGHHLGKD FTPAAQAAF- QKVVAGVATA 150
pHemA.pep 101 HAHKLRVDPV NFKLLSHCLL VTLAAHHPDD FNPSVHASLD -KFLANVSTV 150
pHemB.pep 101 HCDQLHVDPE NFRLLGNVIV VVLARRLGHD FNPDVQAAF- QKVVAGVANA 150
160 170 180 190 200
hHemA.pep 151 LTSKYR.... 200
hHemB.pep 151 LAHKYH.... 200
mHemA.pep 151 LTSKYR.... 200
mHemB.pep 151 LAHKYH.... 200
pHemA.pep 151 LTSKYR.... 200
pHemB.pep 151 LAHKYH.... 200

Fig. 16C

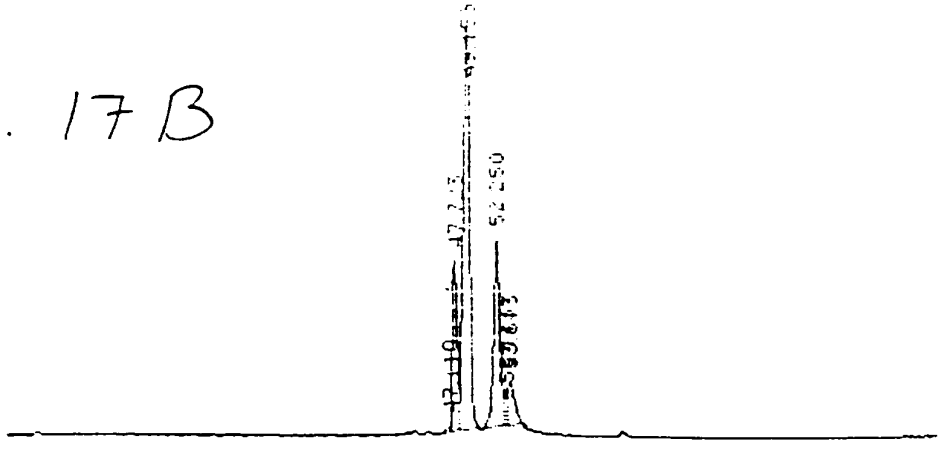
Fig 17A



Analysis: Channel A

Peak No	Time	Type	Height(μV)	Area(μV-sec)	Area%
1	48.200	N	1677	20438	1.515
2	52.076	N1	7625	116593	8.631
3	52.510	N2	32010	881490	65.369
4	53.660	N3	10066	330153	24.487
Total Area				1348474	99.990

Fig. 17B



Analysis: Channel A

Peak No.	Time	Type	Height(μV)	Area(μV-sec)	Area%
1	47.110	N1	1727	24840	0.204
2	47.723	N2	75067	1738939	14.321
3	49.153	N3	188795	6206410	51.114
4	52.250	N1	81476	3046748	25.092
5	53.113	N2	13195	202166	1.664
6	53.613	N3	19211	914954	7.535
	65.753	N	318	8066	0.066
Total Area				12142123	99.996

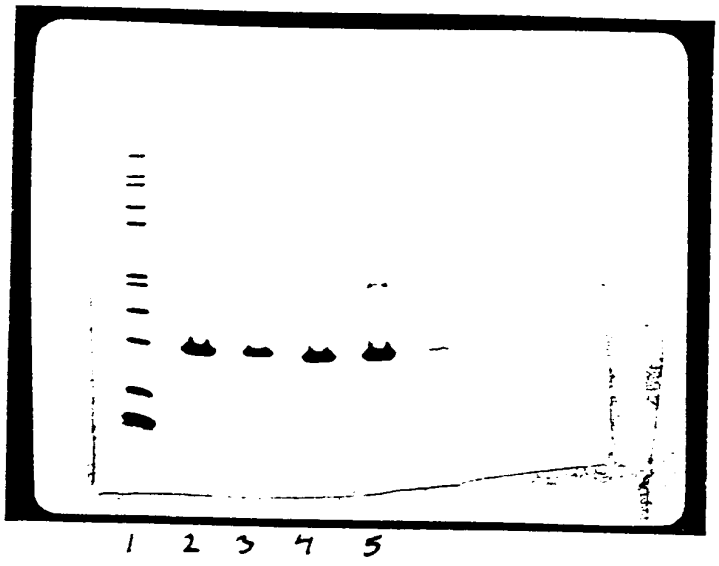


Fig. 18

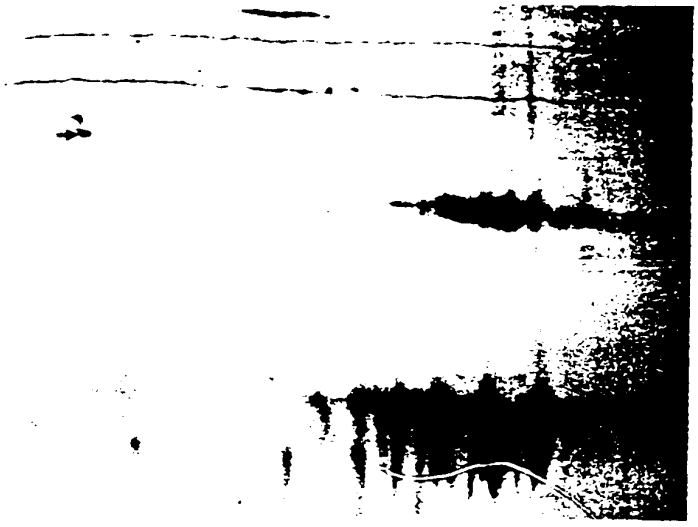


Fig. 19A

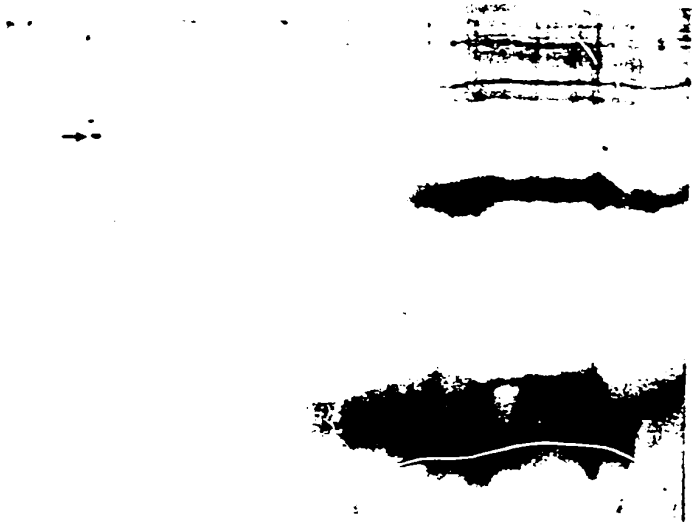


Fig. 19B

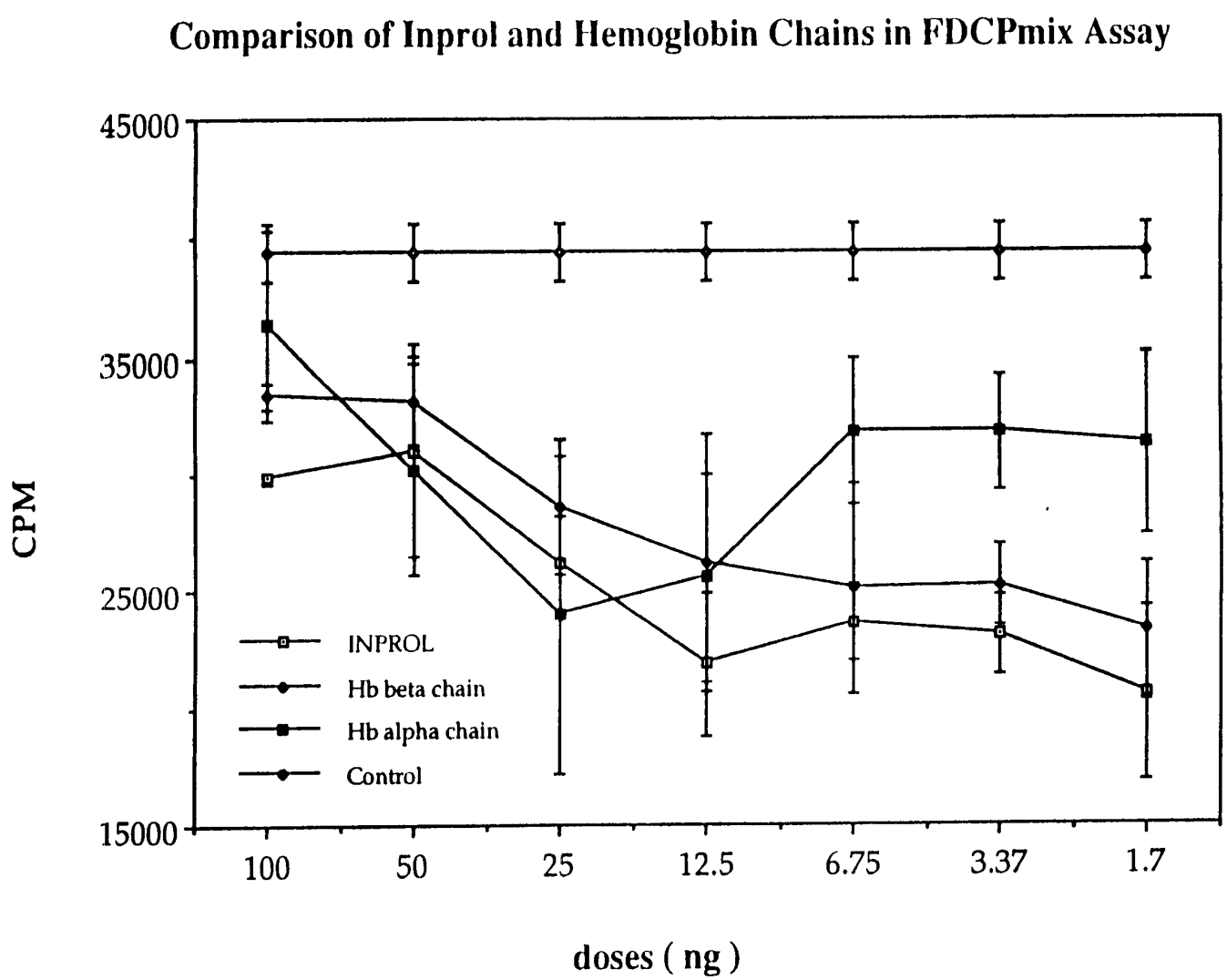

Comparison of Inprol and Hemoglobin Chains in FDCPmix Assay
45000
35000
25000
15000
CPM
INPROL
Hb beta chain
Hb alpha chain
Control
100
50
25
12.5
6.75
3.37
1.7
doses (ng)

Fig. 20